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Atty Dkt. No.: NATH-003 USSN: 10/799,925

AMENDMENT OF THE CLAIMS

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Please amend the claims as follows:

In the Claims:

- 1. (Original) A method of quantifying the amount of a target nucleic acid of less than about 30 nt in length in a sample, said method comprising:
 - a) contacting said sample with at least two ligation domains that are complementary to different domains of said target nucleic to produce a reaction mixture;
 - b) ligating any resultant annealed ligation domains of any resultant ligation oligonucleotide/target nucleic acid complexes in said reaction mixture to produce a pseudotarget nucleic acid; and
 - c) determining the presence of any pseudotarget nucleic acids in said reaction mixture to quantify the amount of said target nucleic acid in said sample.
- 2. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is a ribonucleic acid.
- 3. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid does not exceed about 25 nt in length.
- 4. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is single-stranded.
- 5. (Original) The method according to Claim 1, wherein said target nucleic acid is an siRNA molecule.

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6. (Original) The method according to Claim 5, wherein said siRNA molecule is a shRNA molecule.

- 7. (Withdrawn) The method according to Claim 1, wherein said ligation domains are present on separate oligonucleotides.
- 8. (Withdrawn) The method according to Claim 7, wherein said ligation domains are present on a Combined Oligo.
- (Withdrawn) The method according to Claim 8, wherein said Combined
 Oligo is a linear deoxyribonucleic acid comprising terminal ligation domains.
- 10. (Withdrawn) The method according to Claim 10, wherein said determining does not comprise amplifying said pseudotarget nucleic acid.
- 11. (Withdrawn) The method according to Claim 1, wherein said determining comprises amplifying said pseudotarget nucleic acid.
- (Withdrawn) The method according to Claim 1, wherein said amplifying is by one of PCR, isothermal amplification, rolling circle amplification and branched DNA.
- 13. (Withdrawn) The method according to Claim 1, wherein said quantifying is relative.
- 14. (Withdrawn) The method according to Claim 1, wherein said quantifying is absolute.
- 15. (Withdrawn) The method according to Claim 1, wherein said ligating occurs at a temperature ranging from about 20 to about 45°C.

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- 16. (Withdrawn) The method according to Claim 15, wherein said ligating occurs at a temperature ranging from about 37 to about 42 °C.
- 17. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is a peptide nucleic acid, locked nucleic acid, methylated nucleic acid, nucleic acid conjugate, thio-nucleic acid or morpholino nucleic acid.
- 18. (Original) A method of quantifying an siRNA in a sample, said method comprising:
 - a) contacting said sample with at least two ligation deoxyribooligonucleotides that are complementary to different adjacent domains of said siRNA to produce a reaction mixture;
 - b) ligating any annealed ligation deoxyribo-oligonucleotides of any resultant ligation deoxyribooligonucleotide/siRNA complexes in said reaction mixture to produce a pseudotarget nucleic acid;
 - c) amplifying any pseudotarget nucleic acids in said reaction mixture by PCR; and
 - d) detecting any resultant PCR amplified product to quantitate said siRNA in said sample.
- 19. (Original) The method according to Claim 18, wherein said siRNA is single-stranded.
- 20. (Original) The method according to Claim 18, wherein said siRNA is double-stranded.
- 21. (Original) The method according to Claim 20, wherein said double-stranded siRNA is a short hairpin RNA.

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- 22. (Original) The method according to Claim 18, wherein said quantitating is relative.
- 23. (Original) The method according to Claim 18, wherein said quantitating is absolute.

24-31 (Canceled)

- 32. (New) The method according to Claim 1, wherein said target nucleic acid ranges in length from about 20 to about 23 nt.
- 33. (New) The method according to Claim 5, wherein said siRNA is a duplex structure which ranges in length from about 15 to about 30 bp.
- 34. (New) The method according to Claim 33, wherein said duplex structure which ranges in length from about 20 to about 29 bp.
- 35. (New) The method according to Claim 34, wherein said duplex structure is 21, 22 or 23 bp in length.
- 36. (New) The method according to Claim 20, wherein said siRNA is a duplex structure which ranges in length from about 15 to about 30 bp.
- 37. (New) The method according to Claim 36, wherein said duplex structure which ranges in length from about 20 to about 29 bp.
- 38. (New) The method according to Claim 37, wherein said duplex structure is 21, 22 or 23 bp in length.